WHAT WE CLAIM IS:

1. A method for securely storing genomic information, said method comprising obtaining genomic information of one or more individuals, separating the genomic information into more than one dataset, storing at least one such dataset in a portable storage device, storing the remainder of the datasets in at least one central database, wherein the portable storage device is the property of the one or more individuals whose genomic information is partly contained therein, and wherein the genomic information is rendered informative only when the dataset or datasets stored in the portable storage device is combined with the dataset or datasets stored in the central database or databases.

2. The method according to claim 1 wherein the information of one dataset may at least in part overlap with that of another dataset.

3. The method according to claim 1 or claim 2 wherein the information in at least one dataset maybe encrypted.

4. The method according to any one of claims 1 to 3 wherein the information present in one dataset that is also present in one or more other datasets is encrypted.

5. The method according to any one of claims 1 to 4 wherein the information of at least one dataset is encrypted and one or more other datasets provides one or more keys for decryption.

6. The method according to any one of claims 1 to 5 wherein the information of at least one dataset is encrypted and more than one encryption method is used to encrypt different parts of the information comprising the dataset(s).

7. The method according to any one of claims 1 to 6 wherein said genomic information comprises nucleotide sequence information and/or annotation information.

8. A method for processing genomic information for secure storage wherein said genomic information comprises a representation of the nucleotide sequence of at least part of the genome of at least one individual, said method comprising converting a nucleotide sequence into one or more fragments, representing the nucleotide sequence of one or more of said fragments by means of a unique identifier, denoting the unique identifier representing a fragment by means of a positional

notation according to the position of the represented fragment in the nucleotide sequence, separating at least some of the positional notations(s) and at least some of the unique identifier(s) into at least two data sets, storing at least some of at least one dataset in a portable electronic storage device, and storing at least the remainder of the dataset(s) on

5   at least one central database, wherein the portable storage device is the property of the one or more individuals whose genomic information is partly contained therein, and wherein the genomic information is rendered informative only when the dataset or datasets stored in the portable storage device is combined with the dataset or datasets stored in the central database or databases.

10   9.   A method for processing genomic information for secure storage wherein said genomic information comprises a representation of the nucleotide sequence of at least part of the genome of at least one individual, said method comprising converting a nucleotide sequence into one or more fragments, representing the nucleotide sequence of one or more of said fragments by means of a unique identifier, denoting the unique identifier

15   representing a fragment by means of a positional notation according to the position of the represented fragment in the nucleotide sequence, separating at least some of the positional notation(s) and at least some of the unique identifier(s) into at least two data sets, storing at least some of at least one dataset separately from the remainder of the dataset(s), wherein access to at least some of at least one dataset may be authorised only

20   by and/or is controlled by the one or more individuals whose genomic information is partly contained therein and/or wherein at least some of at least one dataset is the property of the one or more individuals whose genomic information is partly contained therein, and wherein the genomic information is rendered informative only when the datasets are combined.

25   10.   The method according to claim 9 wherein the representation of the sequence of nucleotides of the one or more fragments by a unique identifier is facilitated by means of a method which correlates a string of n characters of a representation of a nucleotide sequence with a unique identifier which identifies that siring.

       11.   The method according to claim 10 wherein said method utilises a lookup table.

30   12.   The method according to any one of claims 9 to 11 wherein the nucleotide sequence is converted into fragments of the same length.

13. The method according to any one of claims 9 to 12 wherein the nucleotide sequence is converted into fragments of varying lengths.

14. The method according to any one of claims 9 to 13 wherein the method comprises or includes randomising the sequence of unique identifiers and their associated positional notations, separating at least some of the positional notations from at least some of the unique identifiers whilst maintaining the association of each unique identifier with its associated positional notation.

15. The method according to claim 14 wherein the association of a given unique identifier with its positional notation is maintained by their relative position within each dataset.

16. The method according to claim 14 wherein the association of a given unique identifier with its positional notation is provided by a unique association identifier.

17. The method according to any one of claims 9 to 16 wherein said unique identifier(s) and/or positional notation(s) and/or association identifier(s) is or are alphanumeric.

18. A method for reducing the informativeness of genomic information for the secure storage of said genomic information, wherein said genomic information comprises representation information comprising a representation of the nucleotide sequence of at least part of the genome of at least one individual and/or annotation information relating to said genome, and wherein said method comprises obtaining genomic information of one or more individuals, randomising the representation of the nucleotide sequence and/or the annotation information according to a process that generates information to unrandomise said representation information and/or annotation information, and separating said representation information and/or annotation information from the information to unrandomise said representation and/or annotation information, wherein access to at least some of said information to unrandomise said representation information and/or annotation information may be authorised only by and/or is controlled by the one or more individuals whose genomic information may thereby be unrandomised and/or wherein at least some of said information to unrandomise said representation and/or annotation information is the property of the one or more individuals whose genomic information may thereby be unrandomised,, and wherein the genomic information is rendered informative only when the representation information

and/or annotation information and the information to unrandomise said representation information and/or annotation information are combined.

19. A method to reduce the informativeness of genomic information wherein said method comprises or includes a method of processing genomic information as herein described with or without reference to the examples herein.

20. A method for processing genomic information substantially as herein described with or without reference to the examples here.

21. A method for increasing the informativeness of stored genomic information, wherein said stored genomic information comprises or includes two or more separately stored datasets, at least one of which is stored in a portable storage device and the remainder of which are stored in at least one central database, and wherein the genomic information of any dataset(s) is uninformative in the absence of the remainder of datasets, said method comprising or including accessing said datasets, and combining the information of said datasets thereby to yield informative genomic information.

22. A method for increasing the informativeness of processed genomic information wherein said processed genomic information is provided in more than one dataset, and wherein at least part of at least one such dataset comprises a randomised representation of the nucleotide sequence of at least part of the genome of at least one individual and/or randomised annotation information relating to said genome, and wherein at least one other dataset comprises at least part of the information required to unrandomise at least part of said representation and/or annotation information, said method comprising or including accessing said dataset(s) comprising at least part of the information required to unrandomise at least part of said representation and/or annotation information, and unrandomising said representation and/or annotation information to yield informative genomic information.

23. A method for increasing the informativeness of stored genomic information, wherein said stored genomic information comprises or includes randomised representation information comprising a randomised representation of the nucleotide sequence of at least part of the genome of at least one individual and/or randomised annotation information relating to said genome(s) and information to unrandomise said representation information and/or annotation information and wherein the representation

information and/or annotation information is stored separately from at least part of the information to unrandomise said representation and/or annotation information, and wherein said method comprises or includes accessing said information to unrandomise said representation information and/or annotation information, unrandomising the representation information and/or the annotation information using said information to unrandomise said representation information and/or annotation information to yield a unrandomised representation of the nucleotide sequence of at least part of the genome of at least one individual and/or randomised annotation information relating to said genome(s).

24.   The method according to claim 22 or claim 23 wherein access to at least some of said information to unrandomise said representation information and/or annotation information may be authorised only by and/or is controlled by the one or more individuals whose genomic information may thereby be unrandomised and/or wherein at least some of said information to unrandomise said representation and/or annotation information is the property of the one or more individuals whose genomic information may thereby be unrandomised.

25.   A method to increase the informativeness of stored genomic information wherein said method comprises or includes a method of processing genomic information as herein described with or without reference to the examples herein.

26.   Processed genomic information wherein said processed genomic information is provided in more than one dataset, and wherein at least part of at least one such dataset comprises a randomised representation of the nucleotide sequence of at least part of the genome of at least one individual and/or randomised annotation information relating to said genome, and wherein at least one other dataset comprises at least part of the information required to unrandomise the representation and/or annotation information.

27.   The genomic information according to claim 26 wherein the dataset comprising at least part of the information required to unrandomise the representation is stored in a portable storage device.

28.   The genomic information according to claim 27 wherein said portable storage device is the property of the individual or individuals whose genomic information may thereby be unrandomised.

29.   Processed genomic information processed in accordance with methods or processes as herein described with or without reference to the examples herein.